

LL1VH

001.1505876.1

LL1VK

GATGTTTGATGACCCCACTCCACTCTCCCTGCTCTCAGTCTTGAGATGAAAGCCCTCCATCTCTTGAGATCTAGTCAAGCCCTTGTA
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 CTACAACTACTCTGCTTGAGGTGAGAGGACGACACGTGAGAACCTCTAGTTGGAGTGAGAAAGCTTAGATCAGTCTCGGAACAT
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 D V V M T Q T P L S L P V S L Q D Q A S I S C R S S Q S L V
 10 20 27A B C

[illegible]

TCTGGGGTCCCAACACAGCTTCAGTCGTCAGTGGATCAGCGACACAGATTTCACACTCAGATTCAGTAGAGTGAGGCTGAGGATCTGGGACTT
 270
 AGACCCCAAGGGTCTGTCTCCAGTCAACCTCACTTAGTCCCTGTCTTAAGTGTGAGTTCTATGTCATCTCACCTCCGACTCCTAGACCCCTGAA
 80
 S G V P D R F S G S G S G T D F T L K I S R V E A E D L G L
 70
 50

337

TATTTTCCTCTCTAAAGTTCACATGTTCCCTCCACAGTTGGTGCTGGAGACCAGGTGGAATCTAAC
-----+-----+-----+-----+-----+-----
ATAAAGACGAGAATTTCCAAGTGTACACAGAGGGTGCACAACCACGACCTGTGTTGCACCTTGATTG
30100

Y P C S Q S S H V P P T F G A G T K L E I

CDR3

CELL 1 VH

001.1505876.1

Figure 2B

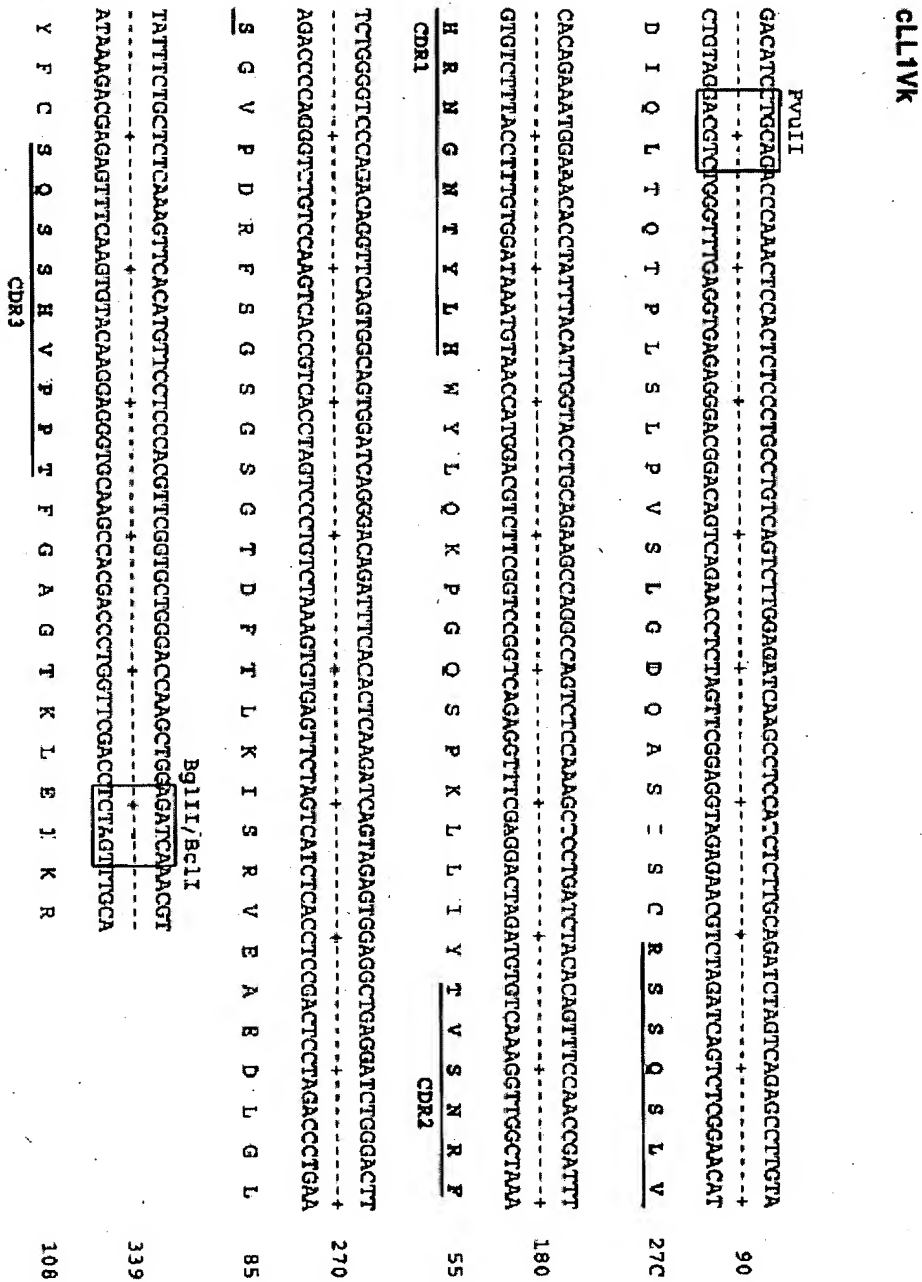


Figure 3A

RF-TS3	QVQLVQSGSELKPGASVKVSCKASGYTFTSYAMN	40
CLL1VH	QVQLQ...P...ET...T...T...N...GV...IK...T	40
hLL1VH	QVQLQ...N...GV...IK...	40
RF-TS3	PGQGLEWMGWINTNTGNTPTYAQGFTGRFVFSLDTSVSTAY	79
CLL1VH	...E...Q...P...E...FDD...A...ES...A...F	79
hLL1VH	...Q...P...E...FDD...A...	79
RF-TS3	LQISSLKADDTAVYYCAR	102
CLL1VH	...N...NE...MGT...F...S...SRGKNEAW...A...	102
hLL1VH	...F...S...SRGKNEAW...A...	102
NEWM	WGQGS�VTSS	113
CLL1VH	...T...TVSS	113
hLL1VH	...TVSS	113

Figure 3B

HF-21/28	DVMTQSPISLPVTLGQPASIS	CRSSQSLVHSDGNTYLNW	35
CLL1VK	DIQLT	SD	35
hLL1VK	<u>DIQL</u>	RN	35

HF-21/28	FQQRPGQSPRLIYKVS	NRDSCGVPDRFSGSGGTDTLKI	75
CLL1VK	YL	KL	75
hLL1VK	L	TF	75

HF-21/28	SRVEAEDVGVYCMQ	GTHWPTFGQTRLEI	106
CLL1VK	L	FS	108
hLL1VK	F	SSVPA	108

HALLOW

001.1505876.1

hLL1vk

001.1505876.1

Figure 5

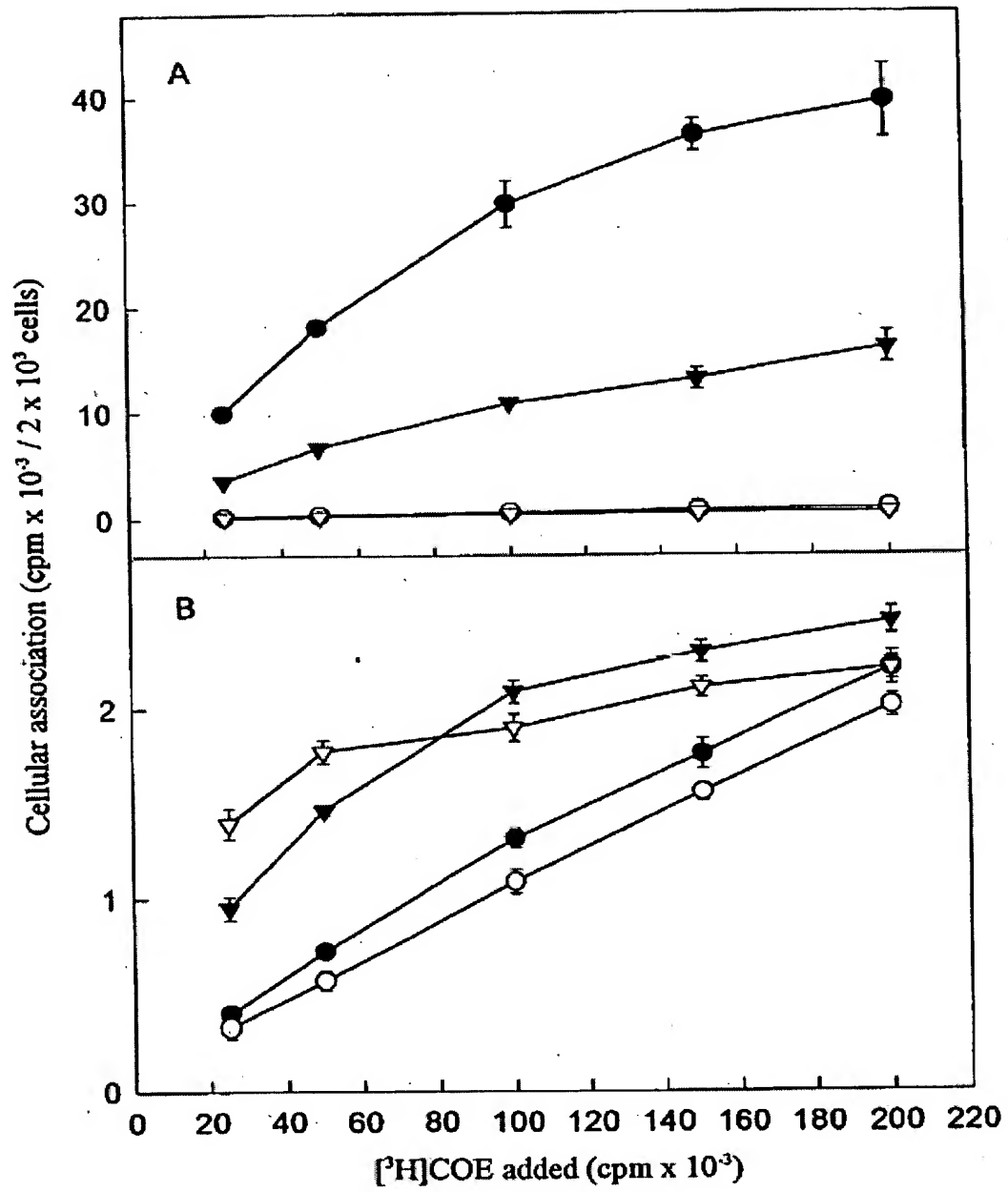


Figure 6

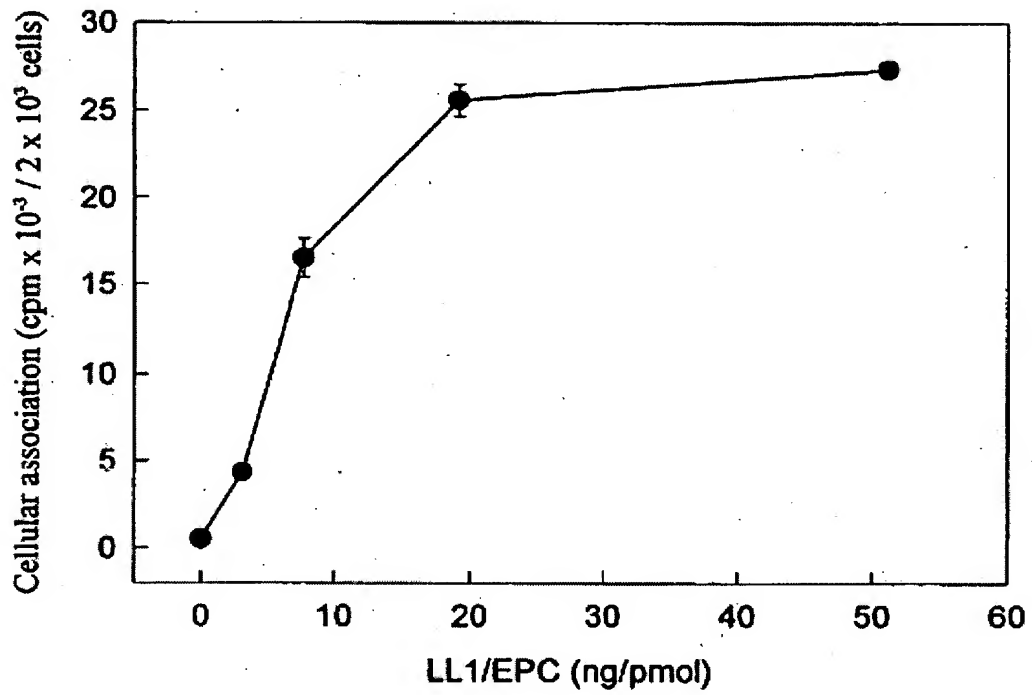


Figure 7

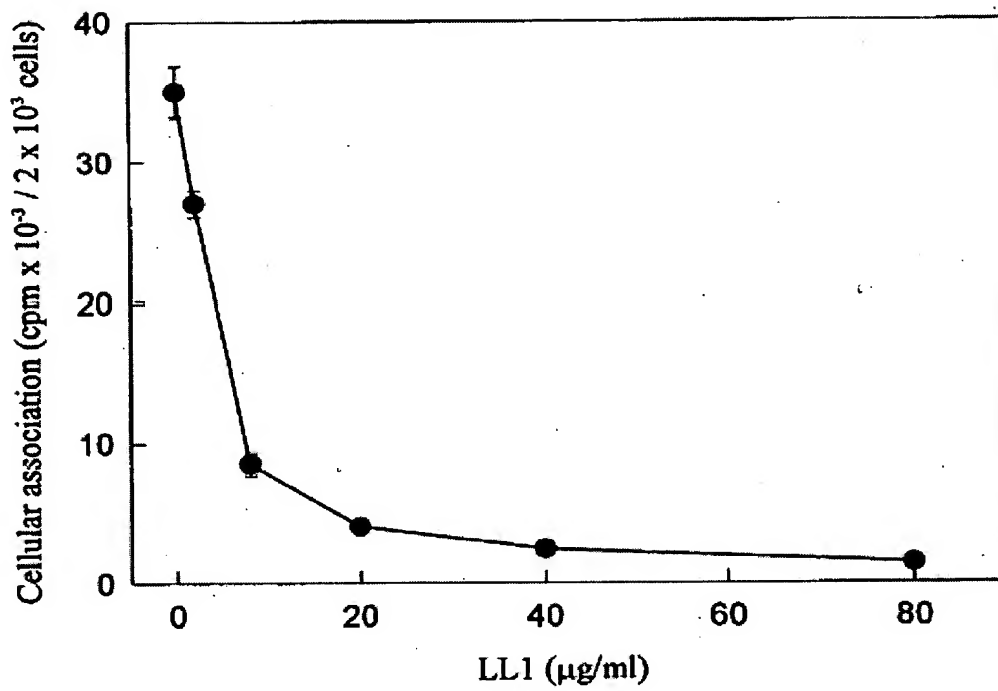


Figure 8

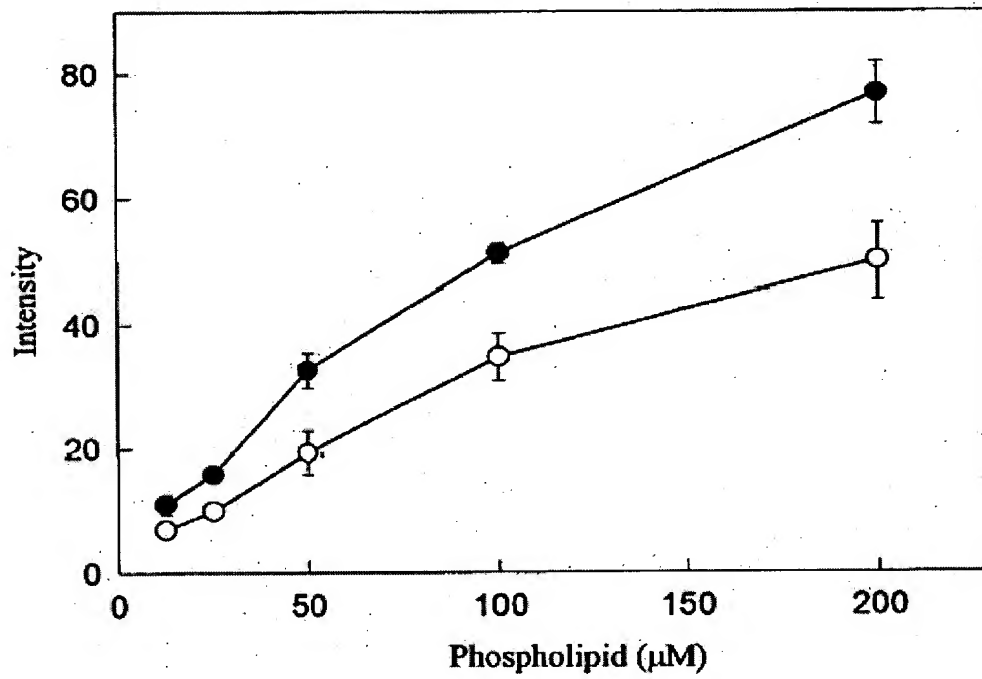


Figure 9

